

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Ish-Horowicz, David  
Henrique, Domingos Manuel Pinto  
Lewis, Julian Hart  
Artavanis-Tsakonas, Spyridon  
Gray, Grace
- (ii) TITLE OF THE INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS  
AND FRAGMENTS
- (iii) NUMBER OF SEQUENCES: 94
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Pennie & Edmonds LLP  
(B) STREET: 1155 Avenue of the Americas  
(C) CITY: New York  
(D) STATE: NY  
(E) COUNTRY: USA  
(F) ZIP: 10036/2711
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: TO BE ASSIGNED  
(B) FILING DATE: ON AN EVEN DATE HEREWITH  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/981,392  
(B) FILING DATE: 22-DEC-1997  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Antler, Adriane M.  
(B) REGISTRATION NUMBER: 32,605  
(C) REFERENCE/DOCKET NUMBER: 7326-122
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 212-790-9090  
(B) TELEFAX: 212-869-8864  
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2508 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 277...2460

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCA CGAGGTTTTT TTTTTTTTTT TTCCCCTCTT TTCTTTCTTT TCCTTTTGCC 60  
ATCCGAAAGA GCTGTGAGCC GCCGCCGGGC TGCACCTAAA GGCGTCGGTA GGGGGATAAC 120  
AGTCAGAGAC CCTCCTGAAA GCAGGAGACG GGACGGTACC CCTCCGGCTC TGCGGGGCGG 180  
CTGCGGCCCC TCCGTTCTTT CCCCCTCCCC GAGAGACACT CTCCTTTCC CCCCACGAAG 240  
ACACAGGGGC AGGAACGCGA GCGCTGCCCC TCCGCC ATG GGA GGC CGC TTC CTG 294  
Met Gly Gly Arg Phe Leu  
1 5

CTG ACG CTC GCC CTC CTC TCG GCG CTG CTG TGC CGC TGC CAG GTT GAC 342  
Leu Thr Leu Ala Leu Leu Ser Ala Leu Leu Cys Arg Cys Gln Val Asp  
10 15 20

GGC TCC GGG GTG TTC GAG CTG AAG CTG CAG GAG TTT GTC AAC AAG AAG 390  
Gly Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys  
25 30 35

GGG CTG CTC AGC AAC CGC AAC TGC TGC CGG GGG GGC GGC CCC GGA GGC 438  
Gly Leu Leu Ser Asn Arg Asn Cys Cys Arg Gly Gly Gly Pro Gly Gly  
40 45 50

GCC GGG CAG CAG CAG TGC GAC TGC AAG ACC TTC TTC CGC GTC TGC CTG 486  
Ala Gly Gln Gln Gln Cys Asp Cys Lys Thr Phe Phe Arg Val Cys Leu  
55 60 65 70

AAG CAC TAC CAG GCC AGC GTC TCC CCC GAG CCG CCC TGC ACC TAC GGC 534  
Lys His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly  
75 80 85

AGC GCC ATC ACC CCC GTC CTC GGC GCC AAC TCC TTC AGC GTC CCC GAC 582  
Ser Ala Ile Thr Pro Val Leu Gly Ala Asn Ser Phe Ser Val Pro Asp  
90 95 100

GGC GCG GGC GGC GCC GAC CCC GCC TTC AGC AAC CCC ATC CGC TTC CCC 630  
Gly Ala Gly Gly Ala Asp Pro Ala Phe Ser Asn Pro Ile Arg Phe Pro  
105 110 115

TTC GGC TTC ACC TGG CCC GGC ACC TTC TCG CTC ATC ATC GAG GCT CTG 678  
Phe Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu  
120 125 130

CAC ACC GAC TCC CCC GAC GAC CTC ACC ACA GAA AAC CCC GAG CGC CTC 726  
His Thr Asp Ser Pro Asp Asp Leu Thr Thr Glu Asn Pro Glu Arg Leu  
135 140 145 150

ATC AGC CGC CTG GCC ACC CAG AGG CAC CTG GCG GTG GGC GAG GAG TGG 774  
Ile Ser Arg Leu Ala Thr Gln Arg His Leu Ala Val Gly Glu Glu Trp



AAC CCT GAT GGT GGA TAC AGC TGC CGC TGC CCA CTG GGT TAT TCT GGG	1494
Asn Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro Leu Gly Tyr Ser Gly	
395 400 405	
TTC AAC TGT GAA AAG AAA ATC GAT TAC TGC AGT TCC AGC CCT TGT GCT	1542
Phe Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ala	
410 415 420	
AAT GGA GCC CAG TGC GTT GAC CTG GGG AAC TCC TAC ATA TGC CAG TGC	1590
Asn Gly Ala Gln Cys Val Asp Leu Gly Asn Ser Tyr Ile Cys Gln Cys	
425 430 435	
CAG GCT GGC TTC ACT GGC AGG CAC TGT GAC GAC AAC GTG GAC GAT TGC	1638
Gln Ala Gly Phe Thr Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys	
440 445 450	
GCC TCC TTC CCC TGC GTC AAT GGA GGG ACC TGT CAG GAT GGG GTC AAC	1686
Ala Ser Phe Pro Cys Val Asn Gly Gly Thr Cys Gln Asp Gly Val Asn	
455 460 465 470	
GAC TAC TCC TGC ACC TGC CCC CCG GGA TAC AAC GGG AAG AAC TGC AGC	1734
Asp Tyr Ser Cys Thr Cys Pro Pro Gly Tyr Asn Gly Lys Asn Cys Ser	
475 480 485	
ACG CCG GTG AGC AGA TGC GAG CAC AAC CCC TGC CAC AAT GGG GCC ACC	1782
Thr Pro Val Ser Arg Cys Glu His Asn Pro Cys His Asn Gly Ala Thr	
490 495 500	
TGC CAC GAG AGA AGC AAC CGC TAC GTG TGC GAG TGC GCT CGG GGC TAC	1830
Cys His Glu Arg Ser Asn Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr	
505 510 515	
GGC GGC CTC AAC TGC CAG TTC CTG CTC CCC GAG CCA CCT CAG GGG CCG	1878
Gly Gly Leu Asn Cys Gln Phe Leu Leu Pro Glu Pro Pro Gln Gly Pro	
520 525 530	
GTC ATC GTT GAC TTC ACC GAG AAG TAC ACA GAG GGC CAG AAC AGC CAG	1926
Val Ile Val Asp Phe Thr Glu Lys Tyr Thr Glu Gly Gln Asn Ser Gln	
535 540 545 550	
TTT CCC TGG ATC GCA GTG TGC GCC GGG ATT ATT CTG GTC CTC ATG CTG	1974
Phe Pro Trp Ile Ala Val Cys Ala Gly Ile Ile Leu Val Leu Met Leu	
555 560 565	
CTG CTG GGT TGC GCC GCC ATC GTC GTC TGC GTC AGG CTG AAG GTG CAG	2022
Leu Leu Gly Cys Ala Ala Ile Val Val Cys Val Arg Leu Lys Val Gln	
570 575 580	
AAG AGG CAC CAC CAG CCC GAG GCC TGC AGG AGT GAA ACG GAG ACC ATG	2070
Lys Arg His His Gln Pro Glu Ala Cys Arg Ser Glu Thr Glu Thr Met	
585 590 595	
AAC AAC CTG GCG AAC TGC CAG CGC GAG AAG GAC ATC TCC ATC AGC GTC	2118
Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Ile Ser Val	
600 605 610	
ATC GGT GCC ACT CAG ATT AAA AAC ACA AAT AAG AAA GTA GAC TTT CAC	2166
Ile Gly Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Val Asp Phe His	

615	620	625	630	
AGC GAT AAC TCC	GAT AAA AAC GGC	TAC AAA GTT AGA	TAC CCA TCA GTG	2214
Ser Asp Asn Ser	Asp Lys Asn Gly	Tyr Lys Val Arg	Tyr Pro Ser Val	
	635	640	645	
GAT TAC AAT TTG	GTG CAT GAA CTC	AAG AAT GAG GAC	TCT GTG AAA GAG	2262
Asp Tyr Asn Leu	Val His Glu Leu	Lys Asn Glu Asp	Ser Val Lys Glu	
	650	655	660	
GAG CAT GGC AAA	TGC GAA GCC AAG	TGT GAA ACG TAT	GAT TCA GAG GCA	2310
Glu His Gly Lys	Cys Glu Ala Lys	Cys Glu Thr Tyr	Asp Ser Glu Ala	
	665	670	675	
GAA GAG AAA AGC	GCA GTA CAG CTA	AAA AGT AGT GAC	ACT TCT GAA AGA	2358
Glu Glu Lys Ser	Ala Val Gln Leu	Lys Ser Ser Asp	Thr Ser Glu Arg	
	680	685	690	
AAA CGG CCA GAT	TCA GTA TAT TCC	ACT TCA AAG GAC	ACA AAG TAC CAG	2406
Lys Arg Pro Asp	Ser Val Tyr Ser	Thr Ser Lys Asp	Thr Lys Tyr Gln	
	695	700	705	710
TCG GTG TAC GTC	ATA TCA GAA GAG	AAA GAT GAG TGC	ATC ATA GCA ACT	2454
Ser Val Tyr Val	Ile Ser Glu Glu	Lys Asp Glu Cys	Ile Ile Ala Thr	
	715	720	725	
GAG GTG TAAAACAGAC	GTGACGTGGC AAAGCTTATC	GATACCGTCA TCAAGCTT		2508
Glu Val				

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Gly	Arg	Phe	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Ser	Ala	Leu	Leu
1				5					10					15	
Cys	Arg	Cys	Gln	Val	Asp	Gly	Ser	Gly	Val	Phe	Glu	Leu	Lys	Leu	Gln
			20					25					30		
Glu	Phe	Val	Asn	Lys	Lys	Gly	Leu	Ser	Asn	Arg	Asn	Cys	Cys	Arg	
		35					40				45				
Gly	Gly	Gly	Pro	Gly	Gly	Ala	Gly	Gln	Gln	Gln	Cys	Asp	Cys	Lys	Thr
		50				55					60				
Phe	Phe	Arg	Val	Cys	Leu	Lys	His	Tyr	Gln	Ala	Ser	Val	Ser	Pro	Glu
65					70					75				80	
Pro	Pro	Cys	Thr	Tyr	Gly	Ser	Ala	Ile	Thr	Pro	Val	Leu	Gly	Ala	Asn
			85						90				95		
Ser	Phe	Ser	Val	Pro	Asp	Gly	Ala	Gly	Gly	Ala	Asp	Pro	Ala	Phe	Ser
			100					105					110		
Asn	Pro	Ile	Arg	Phe	Pro	Phe	Gly	Phe	Thr	Trp	Pro	Gly	Thr	Phe	Ser

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115	120	125
Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp Asp Leu Thr Thr		
130	135	140
Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Ala Thr Gln Arg His Leu		
145	150	155
Ala Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg Thr		
165	170	175
Asp Leu Lys Tyr Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr Gly		
180	185	190
Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp Arg Phe Gly His		
195	200	205
Phe Thr Cys Gly Glu Arg Gly Glu Lys Val Cys Asn Pro Gly Trp Lys		
210	215	220
Gly Gln Tyr Cys Thr Glu Pro Ile Cys Leu Pro Gly Cys Asp Glu Gln		
225	230	235
His Gly Phe Cys Asp Lys Pro Gly Glu Cys Lys Cys Arg Val Gly Trp		
245	250	255
Gln Gly Arg Tyr Cys Asp Glu Cys Ile Arg Tyr Pro Gly Cys Leu His		
260	265	270
Gly Thr Cys Gln Gln Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly		
275	280	285
Gly Leu Phe Cys Asn Gln Asp Leu Asn Tyr Cys Thr His His Lys Pro		
290	295	300
Cys Lys Asn Gly Ala Thr Cys Thr Asn Thr Gly Gln Gly Ser Tyr Thr		
305	310	315
Cys Ser Cys Arg Pro Gly Tyr Thr Gly Ser Ser Cys Glu Ile Glu Ile		
325	330	335
Asn Glu Cys Asp Ala Asn Pro Cys Lys Asn Gly Gly Ser Cys Thr Asp		
340	345	350
Leu Glu Asn Ser Tyr Ser Cys Thr Cys Pro Pro Gly Phe Tyr Gly Lys		
355	360	365
Asn Cys Glu Leu Ser Ala Met Thr Cys Ala Asp Gly Pro Cys Phe Asn		
370	375	380
Gly Gly Arg Cys Thr Asp Asn Pro Asp Gly Gly Tyr Ser Cys Arg Cys		
385	390	395
Pro Leu Gly Tyr Ser Gly Phe Asn Cys Glu Lys Lys Ile Asp Tyr Cys		
405	410	415
Ser Ser Ser Pro Cys Ala Asn Gly Ala Gln Cys Val Asp Leu Gly Asn		
420	425	430
Ser Tyr Ile Cys Gln Cys Gln Ala Gly Phe Thr Gly Arg His Cys Asp		
435	440	445
Asp Asn Val Asp Asp Cys Ala Ser Phe Pro Cys Val Asn Gly Gly Thr		
450	455	460
Cys Gln Asp Gly Val Asn Asp Tyr Ser Cys Thr Cys Pro Pro Gly Tyr		
465	470	475
Asn Gly Lys Asn Cys Ser Thr Pro Val Ser Arg Cys Glu His Asn Pro		
485	490	495
Cys His Asn Gly Ala Thr Cys His Glu Arg Ser Asn Arg Tyr Val Cys		
500	505	510
Glu Cys Ala Arg Gly Tyr Gly Gly Leu Asn Cys Gln Phe Leu Leu Pro		
515	520	525
Glu Pro Pro Gln Gly Pro Val Ile Val Asp Phe Thr Glu Lys Tyr Thr		
530	535	540
Glu Gly Gln Asn Ser Gln Phe Pro Trp Ile Ala Val Cys Ala Gly Ile		
545	550	555
Ile Leu Val Leu Met Leu Leu Leu Gly Cys Ala Ala Ile Val Val Cys		
565	570	575

Val Arg Leu Lys Val Gln Lys Arg His His Gln Pro Glu Ala Cys Arg  
580 585 590  
Ser Glu Thr Glu Thr Met Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys  
595 600 605  
Asp Ile Ser Ile Ser Val Ile Gly Ala Thr Gln Ile Lys Asn Thr Asn  
610 615 620  
Lys Lys Val Asp Phe His Ser Asp Asn Ser Asp Lys Asn Gly Tyr Lys  
625 630 635 640  
Val Arg Tyr Pro Ser Val Asp Tyr Asn Leu Val His Glu Leu Lys Asn  
645 650 655  
Glu Asp Ser Val Lys Glu Glu His Gly Lys Cys Glu Ala Lys Cys Glu  
660 665 670  
Thr Tyr Asp Ser Glu Ala Glu Glu Lys Ser Ala Val Gln Leu Lys Ser  
675 680 685  
Ser Asp Thr Ser Glu Arg Lys Arg Pro Asp Ser Val Tyr Ser Thr Ser  
690 695 700  
Lys Asp Thr Lys Tyr Gln Ser Val Tyr Val Ile Ser Glu Glu Lys Asp  
705 710 715 720  
Glu Cys Ile Ile Ala Thr Glu Val  
725

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGGCA	CGAGGTTTTT	TTTTTTTTTT	TTCCCCTCTT	TTCTTTCTTT	TCCTTTTGCC	60
ATCCGAAAGA	GCTGTCTAGC	GCCGCCGGGC	TGCACCTAAA	GGCGTCGGTA	GGGGGATAAC	120
AGTCAGAGAC	CCTCCTGAAA	GCAGGAGACG	GGACGGTACC	CCTCCGGCTC	TGCGGGGCGG	180
CTGCGGCCCC	TCCGTTCTTT	CCCCCTCCCC	GAGAGACACT	CTTCCTTTCC	CCCCACGAAG	240
ACACAGGGGC	AGGAACGCGA	GCGCTGCCCC	TCCGCCATGG	GAGGCCGCTT	CCTGCTGACG	300
CTCGCCCTCC	TCTCGGCGCT	GCTGTGCCGC	TGCCAGGTTG	ACGGCTCCGG	GGTGTTTCGAG	360
CTGAAGCTGC	AGGAGTTTGT	CAACAAGAAG	GGGCTGCTCA	GCAACCGCAA	CTGCTGCCGG	420
GGGGGCGGCC	CCGGAGGCGC	CGGGCAGCAG	CAGTGCGACT	GCAAGACCTT	CTTCCGCGTC	480
TGCCTGAAGC	ACTACCAGGC	CAGCGTCTCC	CCCAGCCGCG	CCTGCACCTA	CGGCAGCGCC	540
ATCACCCCCG	TCCTCGGCGC	CAACTCCTTC	AGCGTCCCCG	ACGGCGCGGG	CGGCGCCGAC	600
CCCGCCTTCA	GCAACCCCAT	CCGCTTCCCC	TTCGGCTTCA	CCTGGCCCCG	CACCTTCTCG	660
CTCATCATCG	AGGCTCTGCA	CACCGACTCC	CCCAGCAGCC	TCACCACAGA	AAACCCCGAG	720
CGCCTCATCA	GCCGCCTGGC	CACCCAGAGG	CACCTGGCGG	TGGGCGAGGA	GTGGTCCCAG	780
GACCTGCACA	GCAGCGGCCG	CACCGACCTC	AAGTACTCCT	ATCGCTTTGT	GTGTGATGAG	840
CACTACTACG	GGGAAGGCTG	CTCTGTCTTC	TGCCGGCCCC	GTGACGACCG	CTTCGGTCAC	900
TTCACCTGTG	GAGAGCGTGG	CGAGAAGGTC	TGCAACCCAG	GCTGGAAGGG	CCAGTACTGC	960
ACTGAGCCGA	TTTGCTTGCC	TGGGTGTGAC	GAGCAGCACG	GCTTCTGCGA	CAAACCTGGG	1020
GAATGCAAGT	GCAGAGTGGG	TTGGCAGGGG	CGGTACTGTG	ACGAGTGCAT	CCGATACCCA	1080
GGCTGCCTGC	ACGGTACCTG	TCAGCAGCCA	TGGCAGTGCA	ACTGCCAGGA	AGGCTGGGGC	1140
GGCCTTTTCT	GCAACCAGGA	CCTGAACTAC	TGCACTCACC	ACAAGCCATG	CAAGAATGGT	1200
GCCACATGCA	CCAACACCGG	TCAGGGGAGC	TACACTTGTT	CTTGCCGACC	TGGGTACACA	1260
GGCTCCAGCT	GCGAGATTGA	AATCAACGAA	TGTGATGCCA	ACCCTTGCAA	GAATGGTGGA	1320
AGCTGCACGG	ATCTCGAGAA	CAGCTATTCC	TGTACCTGCC	CCCCAGGCTT	CTATGGTAAA	1380
AACTGTGAGC	TGAGTGCAAT	GACTTGTGCT	GATGGACCGT	GCTTCAATGG	AGGGCGATGC	1440
ACTGACAACC	CTGATGGTGG	ATACAGCTGC	CGCTGCCCAC	TGGGTTATTG	TGGGTTCAAC	1500

TGTGAAAAGA	AAATCGATTA	CTGCAGTTCC	AGCCCTTGTG	CTAATGGAGC	CCAGTGC GTT	1560
GACCTGGGGA	ACTCCTACAT	ATGCCAGTGC	CAGGCTGGCT	TCACTGGCAG	GCACTGTGAC	1620
GACAACGTGG	ACGATTGCGC	CTCCTTCCCC	TGCGTCAATG	GAGGGACCTG	TCAGGATGGG	1680
GTCAACGACT	ACTCCTGCAC	CTGCCCCCCG	GGATACAACG	GGAAGAACTG	CAGCACGCCG	1740
GTGAGCAGAT	GCGAGCACAA	CCCCTGCCAC	AATGGGGCCA	CCTGCCACGA	GAGAAGCAAC	1800
CGCTACGTGT	GCGAGTGC GC	TCGGGGCTAC	GGCGGCCCTCA	ACTGCCAGTT	CCTGCTCCCC	1860
GAGCCACCTC	AGGGGCCGGT	CATCGTTGAC	TTCACCGAGA	AGTACACAGA	GGGCCAGAAC	1920
AGCCAGTTTC	CCTGGATCGC	AGTGTGCGCC	GGGATTATTC	TGGTCCTCAT	GCTGCTGCTG	1980
GGTTGCGCCG	CCATCGTCGT	CTGCGTCAGG	CTGAAGGTGC	AGAAGAGGCA	CCACCAGCCC	2040
GAGGCCTGCA	GGAGTGAAAC	GGAGACCATG	AACAACCTGG	CGAACTGCCA	GCGCGAGAAG	2100
GACATCTCCA	TCAGCGTCAT	CGGTGCCACT	CAGATTAAAA	ACACAAATAA	GAAAGTAGAC	2160
TTTCACAGCG	ATAACTCCGA	TAAAAACGGC	TACAAAGTTA	GATACCCATC	AGTGGATTAC	2220
AATTTGGTGC	ATGAACTCAA	GAATGAGGAC	TCTGTGAAAG	AGGAGCATGG	CAAATGCGAA	2280
GCCAAGTGTG	AAACGTATGA	TTCAGAGGCA	GAAGAGAAAA	GCGCAGTACA	GCTAAAAAGT	2340
AGTGACACTT	CTGAAAGAAA	ACGGCCAGAT	TCAGTATATT	CCACTTCAAA	GGACACAAAG	2400
TACCAGTCGG	TGTACGTCAT	ATCAGAAGAG	AAAGATGAGT	GCATCATAGC	AACTGAGGTT	2460
AGTATCCCA	CTGGCAGTCG	GACAAGTCTT	GGTGTGTGAT	TCCCATCCAG	CGCAGGTCAG	2520
GGCGGCCAAA	CCATTCTACC	TGCTGCCACA	GTCATCTGTA	CCCAATGAAA	ACTGGCCACC	2580
TTCAGTCTGT	GGCACTGCAG	ACGTTGAAAA	AACTTGTGTG	GGATTAACAT	AAGCTCCAGT	2640
GGGGGTTACA	GGGACAGCAA	TTTTTGCAGG	CAAGGGTATA	ACTGTAGTGC	AGTTGTAGCT	2700
TACTAACCTT	ACTGACTCAT	TCTTTCGTGT	GCTTCCTGCA	GAGCCTGTTT	TTGCTTGGCA	2760
TTGAGGTGAA	GTCCTGACCC	TCTGCATCCT	CATAGTCCTC	TGCTTCTTTT	TTATTAACCT	2820
CTTCTGGTCT	CTGCTTGTCT	TTTCTCTCAA	CAGGTGTAAA	ACAGACGTGA	CGTGGCAAAG	2880
CTT						2883

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2857 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCCAGCGGT	ACCATGGGCC	GTCGGAGCGC	GCTACCCCTT	GCCGTGGTCT	CTGCCCTGCT	60
GTGCCAGGTC	TGGAGCTCCG	GCGTATTTGA	GCTGAAGCTG	CAGGAGTTCG	TCAACAAGAA	120
GGGGCTGCTG	GGGAACCGCA	ACTGCTGCCG	CGGGGGCTCT	GGCCCCCTT	GCGCCTGCAG	180
GACCTTCTTT	CGCGTATGCC	TCAACCACTA	CCAGGCCAGC	GTGTCACCGG	AGCCACCCTG	240
CACCTACGGC	AGTGCTGTCA	CGCCAGTGCT	GGGTCTCGAC	TCCTTCAGCC	TGCCTGATGG	300
CGCAGGCATC	GACCCCGCCT	TCAGCAACCC	ATCCGATTCC	CCTTCCGGCT	TCACCTGGCC	360
AGGTACCTTC	TCTCTGATCA	TTGAAGCCCT	CCATACAGAC	TCTCCCGATG	ACCTCGCAAC	420
AGAAAACCCA	GAAAGACTCA	TCAGCCGCCT	GACCACACAG	AGGCACCTCA	CTGTGGGACG	480
AATGGTCTCA	GGACCTTCAC	AGTAGCGGCC	GCACAGACCT	CCGGTACTCT	TACCGGTTTG	540
TGTGTGACGA	GCACTACTAC	GGAGAAGGTT	GCTCTGTGTT	CTGCCGACCT	CGGGATGACG	600
CCTTTGGCCA	CTTCACCTGC	GGGGACAGAG	GGGAGAAGAT	GTGCGACCCT	GGCTGGAAAG	660
GCCAGTACTG	CACTGACCCA	ATCTGTCTGT	CAGGGTGTGA	TGACCAACAT	GGTACTGTG	720
ACAAACCAGG	GGAGTGCAAG	TGCAGAGTTG	GCTGGCAGGG	CCGCTACTGC	GATGAGTGCA	780
TCCGATACCC	AGGTTGTCTC	CATGGCACCT	GCCAGCAACC	CTGGCAGTGT	AACTGCCAGG	840
AAGGCTGGGG	GGGCCTTTTC	TGCAACCAAG	ACCTGAACTA	CTGTACTCAC	CATAAGCCGT	900
GCAGGAATGG	AGCCACCTGC	ACCAACACGG	GCCAGGGGAG	CTACACATGT	TCCTGCCGAC	960
TGGGGTATAC	AGGTGCCAAC	TGTGAGCTGG	AAGTAGATGA	GTGTGCTCCT	AGCCCCCTGCA	1020
AGAACGGAGC	GAGCTGCACG	GACCTTGAGG	ACAGCTTCTC	TTGCACCTGC	CCTCCCGGCT	1080
TCTATGGCAA	GGTCTGTGAG	CTTGAGCGCC	ATGACCTGTG	CAGATGGCCC	TTGCTTCAAT	1140
GGAGGACGAT	GTTCAAGATA	CCCTGACGGA	GGCTACACCT	GCCATTGCCC	CTTGGGCTTC	1200
TCTGGCTTCA	ACTGTGAGAA	GAAGATGGAT	CTCTGCGGCT	CTTCCCCCTT	GTTCTAACGG	1260



TGCCAAGTGT GTGGACCTCG GCAACTCTTA CCTGTGCCGG TGCCAGGCTG GCTTCTCCGG 1320  
 GACCTACTGC GAGGACAATG TGGATGACTG TGCCTCCTCC CCGTGTGCAA ATGGGGGGCAC 1380  
 CTGCCGGGAC AGTGTGAACG ACTTCTCCTC TACCTGCCCA CCTGGCTACA CGGGCAAGAA 1440  
 CTGCAGCGCC CCTGTCAGCA GGTGTGAGTA TGCACCCTGC CATAATGGGG CCACCTGCCA 1500  
 CCAGAGGGGC CAGCGCTACA TGTGTGAGTG CGCCCAGGGC TATGGCGGGC CCAACTGCCA 1560  
 GTTTCGTCTC CCTGAGCCAC CACCAGGGCC CATGGTGGTG GACCTCAGTG AGAGGCATAT 1620  
 GGAGAGCCAG GCGGGGCCCT TCCCCTCGGT GCGGGTGTGT GCCGGGGTGG TGCTTGTCTT 1680  
 CCTGTGTGCTG CTGGGCTGTG CTGCTGTGGT GGTCTGCGTC CGGCTGAAGC TACAGAAAACA 1740  
 CCAGCCTCCA CCTGAACCCCT GTGGGGGAGA GACAGAAACC ATGAACAACC TAGCCAATTG 1800  
 CCAGCGCGAG AAGGACGTTT CTGTTAGCAT CATTGGGGCT ACCCAGATCA AGAACACCAA 1860  
 CAAGAAGGCG GACTTTCACG GGGACCATGG AGCCAAGAAG AGCAGCTTTA AGGTCCGATA 1920  
 CCCCCTGTG GACTATAACC TCGTTCGAGA CCTCAAGGGA GATGAAGCCA CGGTCAGGGA 1980  
 TACACACAGC AAACGTGACA CCAAGTGCCA GTCACAGAGC TCTGCAGGAG AAGAGAAGAT 2040  
 CGCCCCAACA CTTAGGGGTG GGGAGATTCC TGACAGAAAA AGGCCAGAGT CTGTCTACTC 2100  
 TACTTCAAAG GACACCAAGT ACCAGTCGGT GTATGTTCTG TCTGCAGAAA AGGATGAGTG 2160  
 TGTATAGCG ACTGAGCTGT AAGATGGAAG CGATGTGGCA AAATTCCCAT TTCTCTCAA 2220  
 TAAAATTCCA AGGATATAGC CCCGATGAAT GCTGCTGAGA GAGGAAGGGA GAGGAAACCC 2280  
 AGGGACTGCT GCTGAGAACC AGGTTCAAGC GAAGCTGGTT CTCTCAGAGT TAGCAGAGGC 2340  
 GCCCACACT GCCAGCCTAG GCTTTGGCTG CCGCTGGACT GCCTGCTGGT TGTTCCTATT 2400  
 GCACTATGGA CAGTTGCTTT GAAGAGTATA TATTTAAATG GACGAGTGAC TTGATTCATA 2460  
 TACGAAGCAC GCACTGCCCC CACGTCTATC TTGGATTACT ATGAGCCAGT CTTTCCTTGA 2520  
 ACTAGAAACA CAACTGCCTT TATTGTCCTT TTTGATACTG AGATGTGTTT TTTTTTTTCC 2580  
 TAGACGGGAA AAAGAAAACG TGTGTTATTT TTTTGGGATT TGTAATAATA TTTTTCATGA 2640  
 TATCTGTAAA GCTTGAGTAT TTTGTGACGT TCATTTTTTT ATAATTAA TTTTGGTAAA 2700  
 TATGTACAAA GGCACCTCGG GTCTATGTGA CTATATTTTT TTGTATATAA ATGTATTTAT 2760  
 GGAATATTGT GCAAATGTTA TTTGAGTTTT TTACTGTTTT GTTAATGAAG AAATTCATTT 2820  
 TAAAAATATT TTTCCAAAT AAATATAATG AACTACA 2857

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gly Gln Gln Arg Met Leu Thr Leu Leu Val Leu Ser Ala Val Leu  
 1 5 10 15  
 Cys Gln Ile Ser Cys Ser Gly Leu Phe Glu Leu Arg Leu Gln Glu Phe  
 20 25 30  
 Val Asn Lys Lys Gly Leu Leu Gly Asn Met Asn Cys Cys Arg Pro Gly  
 35 40 45  
 Ser Leu Ala Ser Leu Gln Arg Cys Glu Cys Lys Thr Phe Phe Arg Ile  
 50 55 60  
 Cys Leu Lys His Tyr Gln Ser Asn Val Ser Pro Glu Pro Pro Cys Thr  
 65 70 75 80  
 Tyr Gly Gly Ala Val Thr Pro Val Leu Gly Thr Asn Ser Phe Val Val  
 85 90 95  
 Pro Glu Ser Ser Asn Ala Asp Pro Thr Phe Ser Asn Pro Ile Arg Phe  
 100 105 110  
 Pro Phe Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Glu Ala  
 115 120 125  
 Ile His Ala Asp Ser Ala Asp Asp Leu Asn Thr Glu Asn Pro Glu Arg  
 130 135 140

Leu Ile Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu Gln  
 145 150 155 160  
 Trp Ser Gln Asp Leu His Ser Ser Asp Arg Thr Glu Leu Lys Tyr Ser  
 165 170 175  
 Tyr Arg Phe Val Cys Asp Glu Tyr Tyr Gly Glu Gly Cys Ser Asp  
 180 185 190  
 Tyr Cys Arg Pro Arg Asp Asp Ala Phe Gly His Phe Ser Cys Gly Glu  
 195 200 205  
 Lys Gly Glu Lys Leu Cys Asn Pro Gly Trp Lys Gly Leu Tyr Cys Thr  
 210 215 220  
 Glu Pro Ile Cys Leu Pro Gly Cys Asp Glu His His Gly Tyr Cys Asp  
 225 230 235 240  
 Lys Pro Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys  
 245 250 255  
 Asp Glu Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln  
 260 265 270  
 Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn  
 275 280 285  
 Gln Asp Leu Asn Tyr Cys Thr His His Lys Pro Cys Glu Asn Gly Ala  
 290 295 300  
 Thr Cys Thr Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro  
 305 310 315 320  
 Gly Tyr Thr Gly Ser Asn Cys Glu Ile Glu Val Asn Glu Cys Asp Ala  
 325 330 335  
 Asn Pro Cys Lys Asn Gly Gly Ser Cys Ser Asp Leu Glu Asn Ser Tyr  
 340 345 350  
 Thr Cys Ser Cys Pro Pro Gly Phe Tyr Gly Lys Asn Cys Glu Leu Ser  
 355 360 365  
 Ala Met Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Ala  
 370 375 380  
 Asp Asn Pro Asp Gly Gly Tyr Ile Cys Phe Cys Pro Val Gly Tyr Ser  
 385 390 395 400  
 Gly Phe Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser Ser Asn Pro Cys  
 405 410 415  
 Ala Asn Gly Ala Arg Cys Glu Asp Leu Gly Asn Ser Tyr Ile Cys Gln  
 420 425 430  
 Cys Gln Glu Gly Phe Ser Gly Arg Asn Cys Asp Asp Asn Leu Asp Asp  
 435 440 445  
 Cys Thr Ser Phe Pro Cys Gln Asn Gly Gly Thr Cys Gln Asp Gly Ile  
 450 455 460  
 Asn Asp Tyr Ser Cys Thr Cys Pro Pro Gly Tyr Ile Gly Lys Asn Cys  
 465 470 475 480  
 Ser Met Pro Ile Thr Lys Cys Glu His Asn Pro Cys His Asn Gly Ala  
 485 490 495  
 Thr Cys His Glu Arg Asn Asn Arg Tyr Val Cys Gln Cys Ala Arg Gly  
 500 505 510  
 Tyr Gly Gly Asn Asn Cys Gln Phe Leu Leu Pro Glu Lys Pro Val  
 515 520 525  
 Val Val Asp Leu Thr Glu Lys Tyr Thr Glu Gly Gln Ser Gly Gln Phe  
 530 535 540  
 Pro Trp Ile Ala Val Cys Ala Gly Ile Val Leu Val Leu Met Leu Leu  
 545 550 555 560  
 Leu Gly Cys Ala Ala Val Val Val Cys Val Arg Val Arg Val Gln Lys  
 565 570 575  
 Arg Arg His Gln Pro Glu Ala Cys Arg Gly Glu Ser Lys Thr Met Asn  
 580 585 590  
 Asn Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val Ser Phe Ile  
 595 600 605

Gly	Thr	Thr	Gln	Ile	Lys	Asn	Thr	Asn	Lys	Lys	Ile	Asp	Phe	Leu	Ser
610						615					620				
Glu	Ser	Asn	Asn	Glu	Lys	Asn	Gly	Tyr	Lys	Pro	Arg	Tyr	Pro	Ser	Val
625					630					635					640
Asp	Tyr	Asn	Leu	Val	His	Glu	Leu	Lys	Asn	Glu	Asp	Ser	Pro	Lys	Glu
				645					650					655	
Glu	Arg	Ser	Lys	Cys	Glu	Ala	Lys	Cys	Ser	Ser	Asn	Asp	Ser	Asp	Ser
			660					665					670		
Glu	Asp	Val	Asn	Ser	Val	His	Ser	Lys	Arg	Asp	Ser	Ser	Glu	Arg	Arg
		675					680					685			
Arg	Pro	Asp	Ser	Ala	Tyr	Ser	Thr	Ser	Lys	Asp	Thr	Lys	Tyr	Gln	Ser
	690					695					700				
Val	Tyr	Val	Ile	Ser	Asp	Glu	Lys	Asp	Glu	Cys	Ile	Ile	Ala	Thr	Glu
705					710					715					720
Val															

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	His	Trp	Ile	Lys	Cys	Leu	Leu	Thr	Ala	Phe	Ile	Cys	Phe	Thr	Val
1				5					10					15	
Ile	Val	Gln	Val	His	Ser	Ser	Gly	Ser	Phe	Glu	Leu	Arg	Leu	Lys	Tyr
			20					25					30		
Phe	Ser	Asn	Asp	His	Gly	Arg	Asp	Asn	Glu	Gly	Arg	Cys	Cys	Ser	Gly
		35				40						45			
Glu	Ser	Asp	Gly	Ala	Thr	Gly	Lys	Cys	Leu	Gly	Ser	Cys	Lys	Thr	Arg
	50					55					60				
Phe	Arg	Leu	Cys	Leu	Lys	His	Tyr	Gln	Ala	Thr	Ile	Asp	Thr	Thr	Ser
65					70					75					80
Gln	Cys	Thr	Tyr	Gly	Asp	Val	Ile	Thr	Pro	Ile	Leu	Gly	Glu	Asn	Ser
				85					90					95	
Val	Asn	Leu	Thr	Asp	Ala	Gln	Arg	Phe	Gln	Asn	Lys	Gly	Phe	Thr	Asn
			100					105					110		
Pro	Ile	Gln	Phe	Pro	Phe	Ser	Phe	Ser	Trp	Pro	Gly	Thr	Phe	Ser	Leu
		115					120					125			
Ile	Val	Glu	Ala	Trp	His	Asp	Thr	Asn	Asn	Ser	Gly	Asn	Ala	Arg	Thr
	130					135					140				
Asn	Lys	Leu	Leu	Ile	Gln	Arg	Leu	Leu	Val	Gln	Gln	Val	Leu	Glu	Val
145					150					155					160
Ser	Ser	Glu	Trp	Lys	Thr	Asn	Lys	Ser	Glu	Ser	Gln	Tyr	Thr	Ser	Leu
				165					170					175	
Glu	Tyr	Asp	Phe	Arg	Val	Thr	Cys	Asp	Leu	Asn	Tyr	Tyr	Gly	Ser	Gly
			180					185					190		
Cys	Ala	Lys	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Ser	Phe	Gly	His	Ser	Thr
		195					200					205			
Cys	Ser	Glu	Thr	Gly	Glu	Ile	Ile	Cys	Leu	Thr	Gly	Trp	Gln	Gly	Asp
	210					215					220				



Ser Val Asn Asn Ile Cys Ala Ser Ala Ala Ala Ala Ala Ala Ala  
 690 695 700  
 Ala Ala Ala Asp Glu Cys Leu Met Tyr Gly Gly Tyr Val Ala Ser Val  
 705 710 715 720  
 Ala Asp Asn Asn Asn Ala Asn Ser Asp Phe Cys Val Ala Pro Leu Gln  
 725 730 735  
 Arg Ala Lys Ser Gln Lys Gln Leu Asn Thr Asp Pro Thr Leu Met His  
 740 745 750  
 Arg Gly Ser Pro Ala Gly Thr Ser Ala Lys Gly Ala Ser Gly Gly Gly  
 755 760 765  
 Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser Val Leu Gly Glu Gly Ser  
 770 775 780  
 Tyr Cys Ser Gln Arg Trp Pro Ser Leu Ala Ala Ala Gly Val Ala Gly  
 785 790 795 800  
 Asp Leu Phe Ile Gln Leu Met Ala Ala Ala Ser Val Ala Gly Thr Asp  
 805 810 815  
 Gly Thr Ala Gln Gln Gln Arg Ser Val Val Cys Gly Thr Pro His Met  
 820 825 830

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Val Gln Cys Ala Val Thr Tyr Tyr Asn Thr Thr Phe Cys Thr Thr Phe  
 1 5 10 15  
 Cys Arg Pro Arg Asp Asp Gln Phe Gly His Tyr Ala Cys Gly Ser Glu  
 20 25 30  
 Gly Gln Lys Leu Cys Leu Asn Gly Trp Gln Gly Val Asn Cys  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Thr Cys Ala Glu His Tyr Tyr Gly Phe Gly Cys Asn Lys Phe Cys  
 1 5 10 15  
 Arg Pro Arg Asp Asp Phe Phe Thr His His Thr Cys Asp Gln Asn Gly  
 20 25 30  
 Asn Lys Thr Cys Leu Glu Gly Trp Thr Gly Pro Glu Cys  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asn Leu Cys Ser Ser Asn Tyr His Gly Lys Arg Cys Asn Arg Tyr Cys  
1 5 10 15  
Ile Ala Asn Ala Lys Leu His Trp Glu Cys Ser Thr His Gly Val Arg  
20 25 30  
Arg Cys Ser Ala Gly Trp Ser Gly Glu Asp Cys  
35 40

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Thr Cys Ala Arg Asn Tyr Phe Gly Asn Arg Cys Glu Asn Phe Cys  
1 5 10 15  
Asp Ala His Leu Ala Lys Ala Ala Arg Lys Arg Cys Asp Ala Met Gly  
20 25 30  
Arg Leu Arg Cys Asp Ile Gly Trp Met Gly Pro His Cys  
35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...2199
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGCAGGAAT TCSMYCGCAT GCTCCCGGCC GCC ATG GGC CGT CGG AGC GCG CTA  
Met Gly Arg Arg Ser Ala Leu  
1 5

54

GCC CTT GCC GTG GTC TCT GCC CTG CTG TGC CAG GTC TGG AGC TCC GGC 102  
 Ala Leu Ala Val Val Ser Ala Leu Leu Cys Gln Val Trp Ser Ser Gly  
 10 15 20

GTA TTT GAG CTG AAG CTG CAG GAG TTC GTC AAC AAG AAG GGG CTG CTG 150  
 Val Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys Gly Leu Leu  
 25 30 35

GGG AAC CGC AAC TGC TGC CGC GGG GGC TCT GGC CCG CCT TGC GCC TGC 198  
 Gly Asn Arg Asn Cys Cys Arg Gly Gly Ser Gly Pro Pro Cys Ala Cys  
 40 45 50 55

AGG ACC TTC TTT CGC GTA TGC CTC AAG CAC TAC CAG GCC AGC GTG TCA 246  
 Arg Thr Phe Phe Arg Val Cys Leu Lys His Tyr Gln Ala Ser Val Ser  
 60 65 70

CCG GAG CCA CCC TGC ACC TAC GGC AGT GCC GTC ACG CCA GTG CTG GGT 294  
 Pro Glu Pro Pro Cys Thr Tyr Gly Ser Ala Val Thr Pro Val Leu Gly  
 75 80 85

GTC GAC TCC TTC AGC CTG CCT GAT GGC GCA GGC ATC GAC CCC GCC TTC 342  
 Val Asp Ser Phe Ser Leu Pro Asp Gly Ala Gly Ile Asp Pro Ala Phe  
 90 95 100

AGC AAC CCC ATC CGA TTC CCC TTC GGC TTC ACC TGG CCA GGT ACC TTC 390  
 Ser Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro Gly Thr Phe  
 105 110 115

TCT CTG ATC ATT GAA GCC CTC CAT ACA GAC TCT CCC GAT GAC CTC GCA 438  
 Ser Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp Asp Leu Ala  
 120 125 130 135

ACA GAA AAC CCA GAA AGA CTC ATC AGC CGC CTG ACC ACA CAG AGG CAC 486  
 Thr Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Thr Thr Gln Arg His  
 140 145 150

CTC ACT GTG GGA GAA GAA TGG TCT CAG GAC CTT CAC AGT AGC GGC CGC 534  
 Leu Thr Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg  
 155 160 165

ACA GAC CTC CGG TAC TCT TAC CGG TTT GTG TGT GAC GAG CAC TAC TAC 582  
 Thr Asp Leu Arg Tyr Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr  
 170 175 180

GGA GAA GGT TGC TCT GTG TTC TGC CGA CCT CGG GAT GAC GCC TTT GGC 630  
 Gly Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp Ala Phe Gly  
 185 190 195

CAC TTC ACC TGC GGG GAC AGA GGG GAG AAG ATG TGC GAC CCT GGC TGG 678  
 His Phe Thr Cys Gly Asp Arg Gly Glu Lys Met Cys Asp Pro Gly Trp  
 200 205 210 215

AAA GGC CAG TAC TGC ACT GAC CCA ATC TGT CTG CCA GGG TGT GAT GAC 726  
 Lys Gly Gln Tyr Cys Thr Asp Pro Ile Cys Leu Pro Gly Cys Asp Asp  
 220 225 230

CAA CAT GGA TAC TGT GAC AAA CCA GGG GAG TGC AAG TGC AGA GTT GGC	774
Gln His Gly Tyr Cys Asp Lys Pro Gly Glu Cys Lys Cys Arg Val Gly	
235 240 245	
TGG CAG GGC CGC TAC TGC GAT GAG TGC ATC CGA TAC CCA GGT TGT GTC	822
Trp Gln Gly Arg Tyr Cys Asp Glu Cys Ile Arg Tyr Pro Gly Cys Val	
250 255 260	
CAT GGC ACC TGC CAG CAA CCC TGG CAG TGT AAC TGC CAG GAA GGC TGG	870
His Gly Thr Cys Gln Gln Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp	
265 270 275	
GGG GGC CTT TTC TGC AAC CAA GAC CTG AAC TAC TGT ACT CAC CAT AAG	918
Gly Gly Leu Phe Cys Asn Gln Asp Leu Asn Tyr Cys Thr His His Lys	
280 285 290 295	
CCG TGC AGG AAT GGA GCC ACC TGC ACC AAC ACG GGC CAG GGG AGC TAC	966
Pro Cys Arg Asn Gly Ala Thr Cys Thr Asn Thr Gly Gln Gly Ser Tyr	
300 305 310	
ACA TGT TCC TGC CGA CCT GGG TAT ACA GGT GCC AAC TGT GAG CTG GAA	1014
Thr Cys Ser Cys Arg Pro Gly Tyr Thr Gly Ala Asn Cys Glu Leu Glu	
315 320 325	
GTA GAT GAG TGT GCT CCT AGC CCC TGC AAG AAC GGA GCG AGC TGC ACG	1062
Val Asp Glu Cys Ala Pro Ser Pro Cys Lys Asn Gly Ala Ser Cys Thr	
330 335 340	
GAC CTT GAG GAC AGC TTC TCT TGC ACC TGC CCT CCC GGC TTC TAT GGC	1110
Asp Leu Glu Asp Ser Phe Ser Cys Thr Cys Pro Pro Gly Phe Tyr Gly	
345 350 355	
AAG GTC TGT GAG CTG AGC GCC ATG ACC TGT GCA GAT GGC CCT TGC TTC	1158
Lys Val Cys Glu Leu Ser Ala Met Thr Cys Ala Asp Gly Pro Cys Phe	
360 365 370 375	
AAT GGA GGA CGA TGT TCA GAT AAC CCT GAC GGA GGC TAC ACC TGC CAT	1206
Asn Gly Gly Arg Cys Ser Asp Asn Pro Asp Gly Gly Tyr Thr Cys His	
380 385 390	
TGC CCC TTG GGC TTC TCT GGC TTC AAC TGT GAG AAG AAG ATG GAT CTC	1254
Cys Pro Leu Gly Phe Ser Gly Phe Asn Cys Glu Lys Lys Met Asp Leu	
395 400 405	
TGC GGC TCT TCC CCT TGT TCT AAC GGT GCC AAG TGT GTG GAC CTC GGC	1302
Cys Gly Ser Ser Pro Cys Ser Asn Gly Ala Lys Cys Val Asp Leu Gly	
410 415 420	
AAC TCT TAC CTG TGC CGG TGC CAG GCT GGC TTC TCC GGG AGG TAC TGC	1350
Asn Ser Tyr Leu Cys Arg Cys Gln Ala Gly Phe Ser Gly Arg Tyr Cys	
425 430 435	
GAG GAC AAT GTG GAT GAC TGT GCC TCC TCC CCG TGT GCA AAT GGC GGC	1398
Glu Asp Asn Val Asp Asp Cys Ala Ser Ser Pro Cys Ala Asn Gly Gly	
440 445 450 455	



ACC TGC CGG GAC AGT GTG AAC GAC TTC TCC TGT ACC TGC CCA CCT GGC 1446  
Thr Cys Arg Asp Ser Val Asn Asp Phe Ser Cys Thr Cys Pro Pro Gly  
460 465 470

TAC ACG GGC AAG AAC TGC AGC GCC CCT GTC AGC AGG TGT GAG CAT GCA 1494  
Tyr Thr Gly Lys Asn Cys Ser Ala Pro Val Ser Arg Cys Glu His Ala  
475 480 485

CCC TGC CAT AAT GGG GCC ACC TGC CAC CAG AGG GGC CAG CGC TAC ATG 1542  
Pro Cys His Asn Gly Ala Thr Cys His Gln Arg Gly Gln Arg Tyr Met  
490 495 500

TGT GAG TGC GCC CAG GGC TAT GGC GGC CCC AAC TGC CAG TTT CTG CTC 1590  
Cys Glu Cys Ala Gln Gly Tyr Gly Gly Pro Asn Cys Gln Phe Leu Leu  
505 510 515

CCT GAG CCA CCA CCA GGG CCC ATG GTG GTG GAC CTC AGT GAG AGG CAT 1638  
Pro Glu Pro Pro Pro Gly Pro Met Val Val Asp Leu Ser Glu Arg His  
520 525 530 535

ATG GAG AGC CAG GGC GGC CCC TTC CCC TGG GTG GCC GTG TGT GCC GGG 1686  
Met Glu Ser Gln Gly Gly Pro Phe Pro Trp Val Ala Val Cys Ala Gly  
540 545 550

GTG GTG CTT GTC CTC CTG CTG CTG CTG GGC TGT GCT GCT GTG GTG GTC 1734  
Val Val Leu Val Leu Leu Leu Leu Gly Cys Ala Ala Val Val Val  
555 560 565

TGC GTC CGG CTG AAG CTA CAG AAA CAC CAG CCT CCA CCT GAA CCC TGT 1782  
Cys Val Arg Leu Lys Leu Gln Lys His Gln Pro Pro Pro Glu Pro Cys  
570 575 580

GGG GGA GAG ACA GAA ACC ATG AAC AAC CTA GCC AAT TGC CAG CGC GAG 1830  
Gly Gly Glu Thr Glu Thr Met Asn Asn Leu Ala Asn Cys Gln Arg Glu  
585 590 595

AAG GAC GTT TCT GTT AGC ATC ATT GGG GCT ACC CAG ATC AAG AAC ACC 1878  
Lys Asp Val Ser Val Ser Ile Ile Gly Ala Thr Gln Ile Lys Asn Thr  
600 605 610 615

AAC AAG AAG GCG GAC TTT CAC GGG GAC CAT GGA GCC GAG AAG AGC AGC 1926  
Asn Lys Lys Ala Asp Phe His Gly Asp His Gly Ala Glu Lys Ser Ser  
620 625 630

TTT AAG GTC CGA TAC CCC ACT GTG GAC TAT AAC CTC GTT CGA GAC CTC 1974  
Phe Lys Val Arg Tyr Pro Thr Val Asp Tyr Asn Leu Val Arg Asp Leu  
635 640 645

AAG GGA GAT GAA GCC ACG GTC AGG GAT ACA CAC AGC AAA CGT GAC ACC 2022  
Lys Gly Asp Glu Ala Thr Val Arg Asp Thr His Ser Lys Arg Asp Thr  
650 655 660

AAG TGC CAG TCA CAG AGT CTG CAG GAG AAG AGA AGA TCG CCC CAA CAC 2070  
Lys Cys Gln Ser Gln Ser Leu Gln Glu Lys Arg Arg Ser Pro Gln His  
665 670 675

TTA GGG GTG GGG AGA TTC CTG ACA GAA AAC AGG CCA GAG TCT GTC TAC 2118  
 Leu Gly Val Gly Arg Phe Leu Thr Glu Asn Arg Pro Glu Ser Val Tyr  
 680 685 690 695

TCT ACT TCA AAG GAC ACC AAG TAC CAG TCG GTG TAT GTT CTG TCT GCA 2166  
 Ser Thr Ser Lys Asp Thr Lys Tyr Gln Ser Val Tyr Val Leu Ser Ala  
 700 705 710

GAA AAG GAT GAG TGT GTT ATA GCG ACT GAG GTG TAAGATGGAA GCGATGTGGC 2219  
 Glu Lys Asp Glu Cys Val Ile Ala Thr Glu Val  
 715 720

AAAATTCCCA TTTCTCTTAA ATAAAATTCC AAGGATATAG CCCCATGAA TGCTGCTGAG 2279  
 AGAGGAAGGG AGAGGAAACC CAGGGACTGC TGCTGAGAAC CAGGTTTCAGG CGAACGTGGT 2339  
 TCTCTCAGAG TTAGCAGAGG CGCCCGACAC TGCCAGCCTA GGCTTTGGCT GCCGCTGGAC 2399  
 TGCCTGCTGG TTGTTCCCAT TGCACATATG ACAGTTGCTT TGAAGAGTAT ATATTTAAAT 2459  
 GGACGAGTGA CTTGATTTCAT ATAGGAAGCA CGCACTGCCC ACACGTCTAT CTTGGATTAC 2519  
 TATGAGCCAG TCTTTCCTTG AACTAGAAAC ACAACTGCCT TTATTGTCCT TTTTGATACT 2579  
 GAGATGTGTT TTTTTTTTTT CCTAGACGGG AAAAAAGAAAA CGTGTGTTAT TTTTTTTGGG 2639  
 ATTTGTAAAA ATATTTTTTCA TGATTATGGG AGAGCTCCCA ACGCGTTGGA GGT 2692

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Arg Arg Ser Ala Leu Ala Leu Ala Val Val Ser Ala Leu Leu  
 1 5 10 15  
 Cys Gln Val Trp Ser Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe  
 20 25 30  
 Val Asn Lys Lys Gly Leu Leu Gly Asn Arg Asn Cys Cys Arg Gly Gly  
 35 40 45  
 Ser Gly Pro Pro Cys Ala Cys Arg Thr Phe Phe Arg Val Cys Leu Lys  
 50 55 60  
 His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly Ser  
 65 70 75 80  
 Ala Val Thr Pro Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp Gly  
 85 90 95  
 Ala Gly Ile Asp Pro Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe Gly  
 100 105 110  
 Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His Thr  
 115 120 125  
 Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile Ser  
 130 135 140  
 Arg Leu Thr Thr Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser Gln  
 145 150 155 160  
 Asp Leu His Ser Ser Gly Arg Thr Asp Leu Arg Tyr Ser Tyr Arg Phe  
 165 170 175  
 Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys Arg  
 180 185 190

Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Asp Arg Gly Glu  
 195 200 205  
 Lys Met Cys Asp Pro Gly Trp Lys Gly Gln Tyr Cys Thr Asp Pro Ile  
 210 215 220  
 Cys Leu Pro Gly Cys Asp Asp Gln His Gly Tyr Cys Asp Lys Pro Gly  
 225 230 235 240  
 Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu Cys  
 245 250 255  
 Ile Arg Tyr Pro Gly Cys Val His Gly Thr Cys Gln Gln Pro Trp Gln  
 260 265 270  
 Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp Leu  
 275 280 285  
 Asn Tyr Cys Thr His His Lys Pro Cys Arg Asn Gly Ala Thr Cys Thr  
 290 295 300  
 Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly Tyr Thr  
 305 310 315 320  
 Gly Ala Asn Cys Glu Leu Glu Val Asp Glu Cys Ala Pro Ser Pro Cys  
 325 330 335  
 Lys Asn Gly Ala Ser Cys Thr Asp Leu Glu Asp Ser Phe Ser Cys Thr  
 340 345 350  
 Cys Pro Pro Gly Phe Tyr Gly Lys Val Cys Glu Leu Ser Ala Met Thr  
 355 360 365  
 Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Ser Asp Asn Pro  
 370 375 380  
 Asp Gly Gly Tyr Thr Cys His Cys Pro Leu Gly Phe Ser Gly Phe Asn  
 385 390 395 400  
 Cys Glu Lys Lys Met Asp Leu Cys Gly Ser Ser Pro Cys Ser Asn Gly  
 405 410 415  
 Ala Lys Cys Val Asp Leu Gly Asn Ser Tyr Leu Cys Arg Cys Gln Ala  
 420 425 430  
 Gly Phe Ser Gly Arg Tyr Cys Glu Asp Asn Val Asp Asp Cys Ala Ser  
 435 440 445  
 Ser Pro Cys Ala Asn Gly Gly Thr Cys Arg Asp Ser Val Asn Asp Phe  
 450 455 460  
 Ser Cys Thr Cys Pro Pro Gly Tyr Thr Gly Lys Asn Cys Ser Ala Pro  
 465 470 475 480  
 Val Ser Arg Cys Glu His Ala Pro Cys His Asn Gly Ala Thr Cys His  
 485 490 495  
 Gln Arg Gly Gln Arg Tyr Met Cys Glu Cys Ala Gln Gly Tyr Gly Gly  
 500 505 510  
 Pro Asn Cys Gln Phe Leu Leu Pro Glu Pro Pro Gly Pro Met Val  
 515 520 525  
 Val Asp Leu Ser Glu Arg His Met Glu Ser Gln Gly Gly Pro Phe Pro  
 530 535 540  
 Trp Val Ala Val Cys Ala Gly Val Val Leu Val Leu Leu Leu Leu  
 545 550 555 560  
 Gly Cys Ala Ala Val Val Cys Val Arg Leu Lys Leu Gln Lys His  
 565 570 575  
 Gln Pro Pro Pro Glu Pro Cys Gly Gly Glu Thr Glu Thr Met Asn Asn  
 580 585 590  
 Leu Ala Asn Cys Gln Arg Glu Lys Asp Val Ser Val Ser Ile Ile Gly  
 595 600 605  
 Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Ala Asp Phe His Gly Asp  
 610 615 620  
 His Gly Ala Glu Lys Ser Ser Phe Lys Val Arg Tyr Pro Thr Val Asp  
 625 630 635 640  
 Tyr Asn Leu Val Arg Asp Leu Lys Gly Asp Glu Ala Thr Val Arg Asp  
 645 650 655

Thr His Ser Lys Arg Asp Thr Lys Cys Gln Ser Gln Ser Leu Gln Glu  
660 665 670  
Lys Arg Arg Ser Pro Gln His Leu Gly Val Gly Arg Phe Leu Thr Glu  
675 680 685  
Asn Arg Pro Glu Ser Val Tyr Ser Thr Ser Lys Asp Thr Lys Tyr Gln  
690 695 700  
Ser Val Tyr Val Leu Ser Ala Glu Lys Asp Glu Cys Val Ile Ala Thr  
705 710 715 720  
Glu Val

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gly Arg Leu Leu Ala Ser Ala Leu Leu Cys Val Ser Gly Val Phe  
1 5 10 15  
Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys Gly Leu Leu Asn Arg  
20 25 30  
Asn Cys Cys Arg Gly Gly Gly Cys Cys Thr Phe Phe Arg Val Cys Leu  
35 40 45  
Lys His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly  
50 55 60  
Ser Ala Thr Pro Val Leu Gly Ser Phe Ser Pro Asp Gly Ala Gly Asp  
65 70 75 80  
Pro Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro  
85 90 95  
Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp  
100 105 110  
Asp Leu Thr Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Thr Gln Arg  
115 120 125  
His Leu Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg  
130 135 140  
Thr Asp Leu Tyr Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr Gly  
145 150 155 160  
Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp Phe Gly His Phe  
165 170 175  
Thr Cys Gly Arg Gly Glu Lys Cys Pro Gly Trp Lys Gly Gln Tyr Cys  
180 185 190  
Thr Pro Ile Cys Leu Pro Gly Cys Asp Gln His Gly Cys Asp Lys Pro  
195 200 205  
Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu  
210 215 220  
Cys Ile Arg Tyr Pro Gly Cys Val His Gly Thr Cys Gln Gln Pro Trp  
225 230 235 240  
Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp  
245 250 255  
Leu Asn Tyr Cys Thr His His Lys Pro Cys Asn Gly Ala Thr Cys Thr  
260 265 270

Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly Tyr Thr  
 275 280 285  
 Gly Cys Glu Glu Glu Cys Pro Cys Lys Asn Gly Ser Cys Thr Asp Leu  
 290 295 300  
 Glu Ser Ser Cys Thr Cys Pro Pro Gly Phe Tyr Gly Lys Cys Glu Leu  
 305 310 315 320  
 Ser Ala Met Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys  
 325 330 335  
 Asp Asn Pro Asp Gly Gly Tyr Cys Cys Pro Leu Gly Ser Gly Phe Asn  
 340 345 350  
 Cys Glu Lys Lys Asp Cys Ser Ser Pro Cys Asn Gly Ala Cys Val Asp  
 355 360 365  
 Leu Gly Asn Ser Tyr Cys Cys Gln Ala Gly Phe Gly Arg Cys Asp Asn  
 370 375 380  
 Val Asp Asp Cys Ala Ser Pro Cys Asn Gly Gly Thr Cys Asp Val Asn  
 385 390 395 400  
 Asp Ser Cys Thr Cys Pro Pro Gly Tyr Gly Lys Asn Cys Ser Pro Val  
 405 410 415  
 Ser Arg Cys Glu His Pro Cys His Asn Gly Ala Thr Cys His Arg Arg  
 420 425 430  
 Tyr Cys Glu Cys Ala Gly Tyr Gly Gly Asn Cys Gln Phe Leu Leu Pro  
 435 440 445  
 Glu Pro Pro Gly Pro Val Asp Glu Glu Gln Phe Pro Trp Ala Val Cys  
 450 455 460  
 Ala Gly Leu Val Leu Leu Leu Gly Cys Ala Ala Val Val Cys Val  
 465 470 475 480  
 Arg Leu Lys Gln Lys Pro Glu Cys Glu Thr Glu Thr Met Asn Asn Leu  
 485 490 495  
 Ala Asn Cys Gln Arg Glu Lys Asp Ser Ser Ile Gly Ala Thr Gln Ile  
 500 505 510  
 Lys Asn Thr Asn Lys Lys Asp Phe His Asp Lys Lys Val Arg Tyr Pro  
 515 520 525  
 Val Asp Tyr Asn Leu Val Leu Lys Val His Lys Lys Cys Ser Glu Glu  
 530 535 540  
 Lys Ala Leu Arg Lys Arg Pro Ser Val Tyr Ser Thr Ser Lys Asp Thr  
 545 550 555 560  
 Lys Tyr Gln Ser Val Tyr Val Ser Glu Lys Asp Glu Cys Ile Ala Thr  
 565 570 575  
 Glu Val

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TACGATGAAY	AACCTGGCGA	ACTGCCAGCG	TGAGAAGGAC	ATCTCAGTCA	GCATCATCGG	60
GGCYACGTCA	GATCARGAAC	ACCAACAAGA	AGGCGGACTT	YMCASCGGGG	GACCASAGCG	120
TCCGACAAGA	ATGGMTTTC	AGGCCCGCTA	CCCCAGCGTG	GACTATAACT	CGTGCAGGAC	180
CTCAAGGGTG	ACGACACCGC	CGTCAGGACG	TCGCACAGCA	AGCGTGACAC	CAAGTGCCAG	240

TCCCCAGGCT CCTCAGGGAG GAGAAGGGGA CCCCACCAC ACTCAGGGGK TCGGTGCTGC 300  
 GGGCCGGGCT CAGGAGGGGG TACCTGGGGG GTGTCTTCCT GGAACCACTG CTCCGTTTCT 360  
 CTTCCCAAAT GTTCTCATGC ATTCATTGTG GATTTTCTCT ATTTTCCTTT TAGTGGAGAA 420  
 GCATCTGAAA GAAAAAGGCC GGAAGCGGGC TGTTCACCTT CAAAAGACAC CAAGTACCAG 480  
 TCGGTGTACG TCATATCCGA GGAGAAGGAC GAGTGCCTCA TCGCA 525

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr Asp Glu Xaa Pro Gly Glu Leu Pro Ala  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Gly His Leu Ser Gln His His Arg Gly Xaa Val Arg Ser Xaa Thr  
 1 5 10 15  
 Pro Thr Arg Arg Thr Xaa Xaa Arg Gly Thr Xaa Ala Ser Asp Lys  
 20 25 30  
 Asn Gly Phe Gln Gly Pro Leu Pro Gln Arg Gly Leu  
 35 40

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Val Gln Asp Leu Lys Gly Asp Asp Thr Ala Val Arg Thr Ser His  
 1 5 10 15  
 Ser Lys Arg Asp Thr Lys Cys Gln Ser Pro Gly Ser Ser Gly Arg Arg  
 20 25 30  
 Arg Gly Pro Arg Pro His Ser Gly Xaa Ala Cys Cys Gly Pro Gly Ser  
 35 40 45

Gly Gly Gly Thr Trp Gly Val Ser Ser Trp His Cys Ser Val Ser Leu  
 50 55 60  
 Pro Lys Cys Ser His Ala Phe Ile Val Asp Phe Leu Tyr Phe Pro Phe  
 65 70 75 80  
 Ser Gly Glu Ala Ser Glu Arg Lys Arg Pro Asp Ser Gly Cys Ser Thr  
 85 90 95  
 Ser Lys Asp Thr Lys Tyr Gln Ser Val Tyr Val Ile Ser Glu Glu Lys  
 100 105 110  
 Asp Glu Cys Val Ile Ala  
 115

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Met Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val  
 1 5 10 15  
 Ser Ile Ile Gly Ala Thr Ser Asp Gln Glu His Gln Gln Glu Gly Gly  
 20 25 30  
 Leu Xaa Xaa Gly Gly Pro Xaa Pro Thr Arg Met Xaa Phe Lys Ala Arg  
 35 40 45  
 Tyr Pro Ser Val Asp Tyr Asn Ser Cys Arg Thr Ser Arg Val Thr Thr  
 50 55 60  
 Pro Pro Ser Gly Arg Arg Thr Ala Ser Val Thr Pro Ser Ala Ser Pro  
 65 70 75 80  
 Gln Ala Pro Gln Gly Gly Glu Gly Asp Pro Asp His Thr Gln Gly Xaa  
 85 90 95  
 Arg Ala Ala Gly Arg Ala Gln Glu Gly Val Pro Gly Gly Cys Leu Pro  
 100 105 110  
 Gly Thr Thr Ala Pro Phe Leu Phe Pro Asn Val Leu Met His Ser Leu  
 115 120 125  
 Trp Ile Phe Ser Ile Phe Leu Leu Val Glu Lys His Leu Lys Glu Lys  
 130 135 140  
 Gly Arg Thr Arg Ala Val Gln Leu Gln Lys Thr Pro Ser Thr Ser Arg  
 145 150 155 160  
 Cys Thr Ser Tyr Pro Arg Arg Arg Thr Ser Ala Ser Ser  
 165 170

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Xaa Thr Trp Arg Thr Ala Ser Val Arg Arg Thr Ser Gln Ser Ala Ser  
 1 5 10 15  
 Ser Gly Xaa Arg Gln Ile Xaa Asn Thr Asn Lys Lys Ala Asp Phe Xaa  
 20 25 30  
 Xaa Gly Asp Xaa Ser Val Arg Gln Glu Trp Xaa Ser Arg Pro Ala Thr  
 35 40 45  
 Pro Ala Trp Thr Ile Thr Arg Ala Gly Pro Gln Gly  
 50 55 60

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg His Arg Arg Gln Asp Val Ala Gln Gln Ala  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

His Gln Val Pro Val Pro Arg Leu Leu Arg Glu Glu Lys Gly Thr Pro  
 1 5 10 15  
 Thr Thr Leu Arg Gly Cys Val Leu Arg Ala Gly Leu Arg Arg Gly Tyr  
 20 25 30  
 Leu Gly Gly Val Phe Leu Glu Pro Leu Leu Arg Phe Ser Ser Gln Met  
 35 40 45  
 Phe Ser Cys Ile His Cys Gly Phe Ser Leu Phe Ser Phe  
 50 55 60

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:



Lys Lys Lys Ala Gly Leu Gly Leu Phe Asn Phe Lys Lys Arg His Gln  
 1 5 10 15  
 Val Pro Val Gly Val Arg His Ile Arg Gly Glu Gly Arg Val Arg His  
 20 25 30  
 Arg

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Thr Met Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val  
 1 5 10 15  
 Ser Ile Ile Gly Ala Thr Gly Ile Xaa Asn Thr Asn Lys Lys Ala Asp  
 20 25 30  
 Phe Xaa Xaa Gly Asp Xaa Ser Ser Asp Lys Asn Gly Phe Gln Lys Ala  
 35 40 45  
 Arg Tyr Pro Ser Val Asp Tyr Asn Leu Val Gln Asp Leu Lys Gly Asp  
 50 55 60  
 Asp Thr Ala Val Arg Thr Ser His Ser Lys Arg Asp Thr Lys Cys Gln  
 65 70 75 80  
 Ser Pro Gly Ser Ser Gly Arg Arg Arg Gly Pro Arg Pro His Ser Gly  
 85 90 95  
 Xaa Ala Cys Cys Gly Pro Gly Ser Gly Gly Gly Thr Trp Gly Val Ser  
 100 105 110  
 Ser Trp Asn His Cys Ser Val Ser Leu Pro Lys Cys Ser His Ala Phe  
 115 120 125  
 Ile Val Asp Phe Leu Tyr Phe Pro Phe Ser Gly Glu Ala Ser Glu Arg  
 130 135 140  
 Lys Arg Pro Asp Ser Gly Cys Ser Thr Ser Lys Asp Thr Lys Tyr Gln  
 145 150 155 160  
 Ser Val Tyr Val Ile Ser Glu Glu Lys Asp Glu Cys Val Ile Ala  
 165 170 175

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2899 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCCAGCGGT ACCATGGGCC GTCGAGCGC GCTACCCCTT GCCGTGGTCT CTGCCCTGCT 60  
 GTGCCAGGTC TGGAGCTCCG GCGTATTGA GCTGAAGCTG CAGGAGTTCG TCAACAAGAA 120  
 GGGGCTGCTG GGGAAACCGCA ACTGCTGCCG CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG 180  
 GACCTTCTTT CGCGTATGCC TCAACCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG 240

A7

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CACCTACGGC	AGTGCTGTCA	CGCCAGTGCT	GGGTCTCGAC	TCCTTCAGCC	TGCCTSATKG	300
SGYASGSRYC	SMCCYCGAGG	YCKWCRGYAW	CSMYAAGYYY	GATATCGMMY	TYCGGCTTCA	360
CCTGGCCRGG	YACCTTCTCT	CTGATYATTG	AAGCYCTCCA	YACAGAYTCT	CCYGATGACC	420
TCGCAACAGA	AAACCCAGAA	AGACTCATCA	GCCGCCTGRC	CACYCAGAGG	CACCTSACKG	480
TGGGMGARGA	RTGGTCYCAG	GACCTKCACA	GYAGCGGCCG	CACRGACCTC	MRGTACTCYT	540
ACCGSTTYGT	GTGTGACGAR	CACTACTACG	GAGARGGYTG	CTCTGKTKTC	TGCCGWCCYC	600
GGGAYGAYGC	CTTYGGCCAC	TTCACCTGYG	GGGASMGWGG	GGAGAARRTG	TGCRACCCTG	660
GCTGGAAAGG	SCMGTA CTGC	ACWGASCCRA	TCTGYCTGCC	WGGRTGTGAT	GASCARCATG	720
GATWYTGTA	CAAAC CAGG	GARTGCAAGT	GCAGAGTKGG	CTGGCAGGGC	CGSTACTGYG	780
ATGAGTGYAT	CCGYTAYCCA	GGYTGCTCTC	ATGGCACCTG	CCAGCARCCC	TGGCAGTGYA	840
ACTGCCAGGA	AGGNTGGGGG	GGCCTTTTCT	GCAACCARGA	CCTGAACTAC	TGYACWCACC	900
ATAAGCCSTG	CARGAATGGA	GCCACCTGCA	ACMAACACGG	GCCAGGGGGA	GCTACACWTG	960
KTCYTTGGCC	GGNCYKGGGT	AYANAGGGTG	CCAMCTGYGA	AGCTTGGGRA	KTRGAYGAGT	1020
TGTTGMYCCY	AGCCCYTGGY	AAGAACGGAG	SGAGCTKSAC	GGAYCTTCGG	AGRACAGCTW	1080
CTCYTGYACC	TGCCCWCCCG	GCTTCTAYGG	CAARRTCTGT	GARYTGAGYG	CCATGACCTG	1140
TGCRGAYGGC	CCTTGCTTYA	AYGGRGWCW	RTGYTCAGAY	ARCCCYGAYG	GAGGSTACAS	1200
CTGCCRYTGC	CCCKTGGGCT	WCTCYGGCTT	CAACTGTGAG	AAGAARATKG	AYYWCTGCRG	1260
CTCTTCMCCY	TGTTCTAAYG	GTGCCAAGTG	TGTGGACCTC	GGYRAYKCYT	ACCTGTGCCG	1320
STGCCAGGCY	GGCTTCTCSG	GGAGGYACTG	YGASGACAAY	GTGGAYGACT	GYGCCTCCTC	1380
CCCGTGYGCM	AAYGGGGGCA	CCTGCCGGGA	YRGYGTGAAC	GACTTGTCCT	GYACCTGCCC	1440
RCCTGGCTAC	ACGGGCARGA	ACTGCAGYGC	CCCYGYCAGC	AGGTGYGAGC	AYGCACCCTG	1500
CCAYAATGGG	GCCACCTGCC	ACSAGAGGGG	CCASC GCTAY	WTGTGYGAGT	GYGCCCCRRR	1560
CTAYGSGGGY	CCCAACTGCC	ANTTYCTGCT	CCCYGAARCY	GMCCMCCMGG	SCCCAYGGTG	1620
GTGGAAMCTC	MSYKARARRM	AYMTARRAGR	GCCRGGGSGG	GCCCWTCCCC	TKGGTGGYCG	1680
TGTGYGCCGG	GGTSRTSCTT	GTCCTCMTGC	TGCTGTCTGG	CTGTGCTGCT	GTGGTGGTCT	1740
GCGTCCGGCT	GARGCTRCAG	AARCACCRGC	CYCCASCYGA	MCCCTGNSGG	GGRGAGACRG	1800
ARACCATGAA	CAACCTRGNC	AAYTGCCAGC	GYGAGAAGGA	CRTYTCWGTY	AGCATCATYG	1860
GGGNYACSCA	CATCAAGAAC	ACCAACAAGA	AGGCGGACTT	YCACGGGGAC	CAYRGNCCCR	1920
ASAAGARYRG	CTTYAAGGYC	CGMTACCCMR	NKGTGGACTA	TAACCTCGTK	CRRGACCTCA	1980
AGGGWGAYGA	MRCCRCSGTC	AGGGAYRCRC	ACAGCAARCG	TGACACCAAG	TGNCAGYCMC	2040
AGRGCTCYKG	AGGRGARGAG	AAGGGGAYCS	CCGACCMACA	CTYAGGGGGT	GGAGGAAGMW	2100
TCYTGMAMGA	AAAAGGCCRG	ASTYYGGGYY	TRYTCWACTT	TCAAARGACA	ANCMANGTAC	2160
MAGTCGGTGT	NYGTYMTKTC	YGNAGRAGGA	AGGNTGASTG	YGTYATAGGM	RNYTGAGGTN	2220
GTAARNTGGN	AGCGATGTGG	CAANNTTCCC	ATTTCTCKSA	AAKNNNATTC	CMMGGATATA	2280
GCYCCGNTGA	ATGCTKCTGA	GAGAGGAAGG	GAGAGGAAAC	CCAGGGGACTG	YTKYTCAGAA	2340
CCAGGTTTCA	GCGAAGCTGG	TTCTCTCAGA	GTTAGCAGAG	GCGCCCGACA	CTGCCAGCCT	2400
AGGCTTTGGC	TGCCGCTGGA	CTGCCTGCTG	GTTGTTCCCA	TTGCACTATG	GACAGTTGCT	2460
TTGAAGAGTA	TATATTTAAA	TGGACGAGTG	ACTTGATTCA	TATACGAAGC	ACGCACTGCC	2520
CACACGTCTA	TCTTGGATTA	CTATGAGCCA	GTCTTTTCCT	GAACTAGAAA	CACAACTGCC	2580
TTTATTGTCC	TTTTTGATAC	TGAGATGTGT	TTTTTTTTTT	CCTAGACGGG	AAAAAGAAAA	2640
CGTGTGTTAT	TTTTTTGGGA	TTTGTA AAAA	TATTTTTTCAT	GATATCTGTA	AAGCTTGAGT	2700
ATTTTGTGAC	GTTTCATTTT	TTATAATTTA	AATTTTGGTA	AATATGTACA	AAGGCACTTC	2760
GGGTCTATGT	GACTATATTT	TTTTGTATAT	AAATGTATTT	ATGGAATATT	GTGCAAATGT	2820
TATTTGAGTT	TTTTACTGTT	TTGTTAATGA	AGAAATTCAT	TTTAAAAATA	TTTTTCCAAA	2880
ATAAATATAA	TGAAC TACA					2899

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

6A

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1981 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

T

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

His Trp Val Arg Ala Pro Leu Glu Val Asp Gly Ile Asp Lys Leu Asp  
1 5 10 15  
Ile Glu Phe Arg Leu His Leu Ala Gly His Leu Leu Ser Asp Tyr  
20 25 30

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Ser Pro His Arg Phe Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Pro Arg Asn Arg Lys Pro Arg Lys Thr His Gln Pro Pro Gly His Pro  
1 5 10 15  
Glu Ala Pro Asp Gly Gly Arg Gly Val Val Pro Gly Pro Ala Gln Gln  
20 25 30  
Arg Pro His Gly Pro Gln Val Leu Leu Pro Leu Arg Val  
35 40 45

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Arg Thr Leu Leu Arg Arg Gly Leu Leu Arg Phe Pro Ser Pro Gly Arg  
1 5 10 15

Cys Leu Arg Pro Leu His Leu Trp Gly Ala Trp Gly Glu Ser Val Gln  
 20 25 30  
 Pro Trp Leu Glu Arg Ala Leu Leu His Arg Ala Asp Leu Pro Ala Trp  
 35 40 45  
 Met

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ala Ala Trp Ile Leu  
 1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln Thr Arg Gly Met Gln Val Gln Ser Gly Leu Ala Gly Pro Val Leu  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Val Tyr Pro Leu Ser Arg Leu Ser Pro Trp His Leu Pro Ala Ala  
 1 5 10 15  
 Leu Ala Val Gln Leu Pro Gly Arg Xaa Gly Gly Pro Phe Leu Gln Pro  
 20 25 30  
 Gly Pro Glu Leu Leu His Thr Pro  
 35 40

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ala Leu Gln Glu Trp Ser His Leu Gln Gln Thr Arg Ala Arg Gly Ser  
1 5 10 15  
Tyr Thr Trp Ser Leu Ala Gly Leu Gly Tyr Xaa Gly Cys His Leu Arg  
20 25 30  
Ser Leu Gly Ile Gly Arg Val Val Asp Pro Ser Pro Trp  
35 40 45

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Arg Arg Glu Leu Asp Gly Ser Ser Glu Asn Ser Tyr Ser Cys Thr  
1 5 10 15  
Cys Pro Pro Gly Phe Tyr Gly Lys Ile Cys Glu Leu Ser Ala Met Thr  
20 25 30  
Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Ser Asp Pro Asp  
35 40 45  
Gly Gly Tyr Ser Cys Arg Cys Pro Val Gly Tyr Ser Gly Phe Asn Cys  
50 55 60  
Glu Lys Lys Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ser Asn Gly Ala  
65 70 75 80  
Lys Cys Val Asp Leu Gly Asp Ala Tyr Leu Cys Arg Gly Gln Ala Gly  
85 90 95  
Phe Ser Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys Ala Ser Ser  
100 105 110  
Pro Cys Ala Asn Gly Gly Thr Cys Arg Asp Gly Val Asn Asp Phe Ser  
115 120 125  
Cys Thr Cys Pro Pro Gly Tyr Thr Gly Arg Asn Cys Ser Ala Pro Ala  
130 135 140  
Ser Arg Cys Glu His Ala Pro Cys His Asn Gly Ala Thr Cys His Glu  
145 150 155 160  
Arg Gly His Arg Tyr Xaa Cys Glu Cys Ala Arg Ser Tyr Gly Gly Pro  
165 170 175  
Asn Cys Xaa Phe Leu Leu Pro Glu Thr Ala Pro Pro Ala Pro Arg Trp  
180 185 190  
Trp Lys Leu Pro  
195

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Lys Asn Leu Lys Gly Pro Gly Gly Ala His Pro Leu Gly Gly Arg Val  
1 5 10 15  
Arg Arg Gly His Pro Cys Pro His Ala Ala Gly Leu Cys Arg Cys  
20 25 30  
Gly Gly Leu Arg Pro Ala Glu Ala Glu Ala Pro Ala Pro Ser Arg  
35 40 45  
Pro Leu Xaa Gly Gly Asp Gly Asp His Glu Gln Pro Gly Gln Leu Pro  
50 55 60  
Ala  
65

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu Gly His Leu Ser Gln His His Arg Gly His Ala Asp Gln Glu His  
1 5 10 15  
Gln Gln Glu Gly Gly Leu Pro Arg Gly Pro Gln Xaa Arg Gln Glu Trp  
20 25 30  
Leu Gln Gly Pro Leu Pro Xaa Gly Gly Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Pro Arg Ala Gly Pro Gln Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Arg His Arg Arg Gln Gly Arg Ala Gln Gln Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

His Gln Val Xaa Ala Pro Gly Leu Leu Arg Gly Gly Glu Gly Asp Pro  
1 5 10 15  
Arg Pro Thr Leu Arg Gly Trp Arg Lys His Leu Glu Arg Lys Arg Pro  
20 25 30  
Asp Phe Gly Leu Val Gln Leu Ser Lys Asp Xaa Gln Xaa Thr Ser Arg  
35 40 45  
Cys Xaa Ser Phe Pro Xaa Glu Glu Gly  
50 55

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Leu Arg His Arg Xaa Leu Arg Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Xaa Trp Lys Xaa Xaa Pro Gly Phe Arg Phe Gln Ser Phe  
1 5 10

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ile Gly Tyr Gly Pro Pro Ser Arg Ser Thr Val Ser Ile Ser Leu Ile  
1 5 10 15  
Ser Asn Ser Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu  
20 25 30  
Ala Leu His Thr Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu  
35 40 45  
Arg Leu Ile Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu  
50 55 60  
Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr  
65 70 75 80  
Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser  
85 90 95  
Val Phe Cys Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly  
100 105 110  
Glu Arg Gly Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys  
115 120 125  
Thr Glu Pro Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys  
130 135 140  
Asp Lys Pro Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr  
145 150 155 160  
Cys Asp Glu Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln  
165 170 175  
Gln Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys  
180 185 190  
Asn Gln Asp Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly  
195 200 205  
Ala Thr Cys Asn Lys His Gly Pro Gly Gly Ala Thr Leu Gly Leu Trp  
210 215 220  
Pro Xaa Trp Gly Thr Xaa Gly Ala Thr Cys Glu Ala Trp Gly Leu Asp  
225 230 235 240  
Glu Leu Leu Thr Pro Ala Leu Gly Lys Asn Gly Gly Ser Leu Thr Asp  
245 250 255  
Leu Arg Arg Thr Ala Thr Pro Val Pro Ala His Pro Ala Ser Thr Ala  
260 265 270  
Lys Ser Val Asn  
275

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Pro	Val	Arg	Thr	Ala	Leu	Ala	Leu	Thr	Gly	Val	Gly	Ala	Gln	Thr	Ala
1				5					10					15	
Pro	Met	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Pro	Trp	Ala	Thr	Pro	Ala	Ser
		20						25					30		
Thr	Val	Arg	Arg	Lys	Leu	Thr	Thr	Ala	Ala	Leu	His	Pro	Val	Leu	Met
		35				40						45			
Val	Pro	Ser	Val	Trp	Thr	Ser	Val	Met	Pro	Thr	Cys	Ala	Ala	Ala	Arg
	50				55						60				
Pro	Ala	Ser	Arg	Gly	Gly	Thr	Val	Thr	Thr	Thr	Trp	Thr	Thr	Ala	Pro
65				70					75						80
Pro	Pro	Arg	Ala	Pro	Thr	Gly	Ala	Pro	Ala	Gly	Met	Ala			
				85					90						

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Thr	Thr	Ser	Pro	Ala	Pro	Ala	Arg	Leu	Ala	Thr	Arg	Ala	Gly	Thr	Ala
1				5					10					15	
Val	Pro	Pro	Pro	Ala	Gly	Ala	Ser	Thr	His	Pro	Ala	Thr	Met	Gly	Pro
			20					25					30		
Pro	Ala	Thr	Arg	Gly	Ala	Thr	Ala	Ile	Cys	Ala	Ser	Val	Pro	Glu	Ala
		35				40					45				
Thr	Gly	Val	Pro	Thr	Ala	Xaa	Ser	Cys	Pro	Lys	Leu	Pro	Pro	Arg	Pro
	50				55						60				
His	Gly	Gly	Gly	Asn	Ser	Pro	Lys	Lys	Thr						
65				70											

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Lys	Gly	Arg	Gly	Gly	Pro	Ile	Pro	Leu	Val	Asp	Val	Cys	Ala	Gly	Val
1				5				10						15	

Ile Leu Val Leu Met Leu Leu Leu Gly Cys Ala Ala Val Val Val Cys  
 20 25 30  
 Val Arg Leu Arg Leu Gln Lys His Arg Pro Pro Ala Asp Pro Xaa Arg  
 35 40 45  
 Gly Glu Thr Glu Thr Met Asn Asn Leu Xaa Asn Cys Gln Arg Glu Lys  
 50 55 60  
 Asp Ile Ser Val Ser Ile Ile Gly Xaa Thr Gln Ile Lys Asn Thr Asn  
 65 70 75 80  
 Lys Lys Ala Asp Phe His Gly Asp His Ala Asp Lys Asn Gly Phe Lys  
 85 90 95  
 Ala Arg Tyr Pro Xaa Val Asp Tyr Asn Leu Val Gln Asp Leu Lys Gly  
 100 105 110  
 Asp Asp Thr Ala Val Arg Asp Ala His Ser Lys Arg Asp Thr Lys Xaa  
 115 120 125  
 Gln Pro Gln Gly Ser Ser Gly Glu Glu Gly Thr Pro Asp Pro His Ser  
 130 135 140  
 Gly Gly Gly Gly Ser Ile Leu Lys Glu Lys Gly Arg Thr Ser Gly Leu  
 145 150 155 160  
 Phe Asn Phe Gln Lys Thr Xaa Xaa Val Gln Val Gly Val Arg His Phe  
 165 170 175  
 Arg Arg Arg Lys Xaa Asp Cys Val Ile Gly Xaa  
 180 185

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly Xaa Lys Xaa Xaa Val Xaa Xaa Gly Lys Xaa Ser Pro Asp Ser Xaa  
 1 5 10 15  
 Phe Lys Val Phe  
 20

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu Gly Thr Gly Pro Pro Arg Gly Arg Arg Tyr Arg  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Tyr Arg Ile Pro Ala Ser Pro Gly Arg Ala Pro Ser Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Leu Leu Lys Leu Ser Thr Gln Ile Leu Leu Met Thr Ser Gln Gln Lys  
1 5 10 15  
Thr Gln Lys Asp Ser Ser Ala Ala Trp Pro Pro Arg Gly Thr  
20 25 30

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Arg Trp Ala Arg Ser Gly Pro Arg Thr Cys Thr Ala Ala Ala Arg  
1 5 10 15  
Thr Ser Ser Thr Pro Thr Ala Ser Cys Val Thr Asn Thr Thr Thr Glu  
20 25 30  
Arg Ala Ala Pro Phe Ser Ala Val Pro Gly Thr Met Pro Ser Ala Thr  
35 40 45  
Ser Pro Val Cys Ser Val Gly Arg Lys Cys Ala Thr Leu Ala Gly Lys  
50 55 60  
Gly Pro Thr Ala Gln Ser Arg Ser Ala Cys Leu Asp Val Met Ser Ser  
65 70 75 80  
Met Asp Phe Phe Val Thr Asn Gln Asn Ala Ser Ala Glu Trp Ala Gly  
85 90 95  
Arg Ala Gly Thr Val Thr Ser Val Ser Ala Ile Gln Ala Val Ser Met  
100 105 110  
Ala Pro Ala Ser Ser Pro Gly Ser Ala Thr Ala Arg Lys Xaa Gly Gly  
115 120 125

Ala Phe Ser Ala Thr Arg Thr  
130 135

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Thr Thr Ala His Thr Ile Ser Pro Ala Arg Met Glu Pro Pro Ala Thr  
1 5 10 15  
Asn Thr Gly Gln Gly Glu Leu His Leu Val Phe Gly Arg Xaa Gly Val  
20 25 30  
Xaa Arg Val Pro Pro Ala Lys Leu Gly Asp Trp Thr Ser Cys  
35 40 45

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Gln Pro Leu Val Arg Thr Glu Gln Glu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Arg Ile Phe Gly Glu Gln Leu Leu Leu Tyr Leu Pro Thr Arg Leu Leu  
1 5 10 15  
Arg Gln Asn Leu  
20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ile Glu Cys His Asp Leu Cys Gly Arg Pro Leu Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Arg Gly Ser Val Leu Arg Gln Pro Arg Trp Arg Val Gln Leu Pro Leu  
1 5 10 15  
Pro Arg Gly Leu Leu Arg Leu Gln Leu  
20 25

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Leu Leu Gln Leu Phe Thr Leu Phe  
1 5

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Trp Cys Gln Val Cys Gly Pro Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Cys Leu Pro Val Pro Leu Pro Gly Arg Leu Leu Gly Glu Ala Leu  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Arg Gln Arg Gly Arg Leu Arg Leu Leu Pro Val Arg Gln Gly His Leu  
1 5 10 15  
Pro Gly Trp Arg Glu Arg Leu Leu Leu His Leu Pro Ala Trp Leu His  
20 25 30  
Gly Gln Glu Leu Gln Cys Pro Arg Gln Gln Val Arg Ala Arg Thr Leu  
35 40 45  
Pro Gln Trp Gly His Leu Pro Arg Glu Gly Pro Pro Leu Phe Val Arg  
50 55 60  
Val Cys Pro Lys Leu Arg Gly Ser Gln Leu Pro Xaa Pro Ala Pro Arg  
65 70 75 80  
Asn Cys Pro Pro Gly Pro Thr Val Val Glu Thr Pro Leu Lys Lys Pro  
85 90 95  
Lys Arg Ala Gly Gly Gly Pro Ser Pro Trp Trp Thr Cys Ala Pro Gly  
100 105 110  
Ser Ser Leu Ser Ser Cys Cys Cys Trp Ala Val Pro Leu Trp Trp Ser  
115 120 125  
Ala Ser Gly  
130

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gly Cys Arg Ser Thr Gly Pro Gln Pro Thr Pro Xaa Gly Gly Arg Arg  
 1 5 10 15  
 Arg Pro

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Thr Thr Trp Xaa Thr Ala Ser Val Arg Arg Thr Ser Gln Ser Ala Ser  
 1 5 10 15  
 Ser Gly Xaa Arg Arg Ser Arg Thr Pro Thr Arg Arg Arg Thr Ser Thr  
 20 25 30  
 Gly Thr Thr Xaa Pro Thr Arg Met Ala Ser Arg Pro Ala Thr Gln Xaa  
 35 40 45  
 Trp Thr Ile Thr Ser Cys Arg Thr Ser Arg Val Thr Thr Pro Pro Ser  
 50 55 60  
 Gly Thr Arg Thr Ala Ser Val Thr Pro Ser Xaa Ser Pro Arg Ala Pro  
 65 70 75 80  
 Gln Gly Arg Arg Arg Cys Pro Pro Thr His Thr Gln Gly Val Glu Glu  
 85 90 95  
 Ala Ser

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Lys Lys Lys Ala Gly Leu Arg Ala Cys Ser Thr Phe Lys Arg Gln Xaa  
 1 5 10 15  
 Xaa Tyr Lys Ser Val Xaa Val Ile Ser Xaa Gly Gly Arg Xaa Thr Ala  
 20 25 30  
 Ser

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown



(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Glu Xaa Glu Val Val Xaa Trp Xaa Leu Xaa Leu Glu Xaa Xaa Pro Arg  
1 5 10 15  
Ile Pro Xaa Ser Lys Phe  
20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His  
1 5 10 15  
Thr Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile  
20 25 30  
Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser  
35 40 45  
Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg  
50 55 60  
Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys  
65 70 75 80  
Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly  
85 90 95  
Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys Thr Glu Pro  
100 105 110  
Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys Pro  
115 120 125  
Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu  
130 135 140  
Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro Trp  
145 150 155 160  
Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp  
165 170 175  
Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly Ala Thr Cys  
180 185 190

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Thr Asn Thr Gly Gln Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Lys Asn Gly Gly Ser Leu Thr Asp Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Asn Ser Tyr Ser Cys Thr Cys Pro Pro Gly Phe Tyr Gly Lys Ile  
1 5 10 15  
Cys Glu Leu Ser Ala Met Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly  
20 25 30  
Gly Arg Cys Ser Asp Ser Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro  
35 40 45  
Val Gly Tyr Ser Gly Phe Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser  
50 55 60  
Ser Ser Pro Cys Ser Asn Gly Ala Lys Cys Val Asp Leu Gly Asp Ala  
65 70 75 80  
Tyr Leu Cys Arg Cys Gln Ala Gly Phe Ser Gly Arg His Cys Asp Asp  
85 90 95  
Asn Val Asp Asp Cys Ala Ser Ser Pro Cys Ala Asn Gly Gly Thr Cys  
100 105 110  
Arg Asp Gly Val Asn Asp Phe Ser Cys Thr Cys Pro Pro Gly Tyr Thr  
115 120 125  
Gly Arg Asn Cys Ser Ala Pro Ala Ser Arg Cys Glu His Ala Pro Cys  
130 135 140  
His Asn Gly Ala Thr Cys His Glu Arg Gly His Arg Tyr  
145 150 155

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Cys Glu Cys Ala Arg Ser Tyr Gly Gly Pro Asn Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Phe Leu Leu Pro Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Pro Pro Gly Pro  
1

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Leu Leu Gly Cys Ala Ala Val Val Cys Val Arg Leu Arg Leu  
1 5 10 15  
Gln Lys His Arg Pro Pro Ala Asp Pro  
20 25

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Arg Gly Glu Thr Glu Thr Met Asn Asn Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Asn Cys Gln Arg Glu Lys Asp Ile Ser Val Ser Ile Ile Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Thr Gln Ile Lys Asn Thr Asn Lys Lys Ala Asp Phe His Gly Asp His  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ala Asp Lys Asn Gly Phe Lys Ala Arg Tyr Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val Asp Tyr Asn Leu Val Gln Asp Leu Lys Gly Asp Asp Thr Ala Val  
1 5 10 15  
Arg Asp Ala His Ser Lys Arg Asp Thr Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Gln Pro Gln Gly Ser Ser Gly Glu Glu Lys Gly Thr Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Pro Thr Leu Arg  
1

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Arg Lys Arg Pro

1

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 12
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTCGGNTTYA CNTGGCCNGG NAC

23

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: N=Inosine

(A) NAME/KEY: Modified Base  
(B) LOCATION: 12  
(D) OTHER INFORMATION: N=Inosine

(A) NAME/KEY: Modified Base  
(B) LOCATION: 15  
(D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TCNATGCANG TNCCNCCRTT

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe Gly Phe Thr Trp Pro Gly Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Asn Gly Gly Thr Cys Ile Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Ser Ile Pro Pro Gly Ser Arg Thr Ser Leu Gly Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 15
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGNTTCACNT GGCCNGGNAC NTT

23

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: N=Inosine



- (A) NAME/KEY: Modified Base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTNCCNCCRT TYTTRCANGG RTT

23

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Asn Pro Cys Lys Asn Gly Gly Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 15
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ACNATGAAYA AYCTNGCNAA YTG

23

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Thr Met Asn Asn Leu Ala Asn Cys  
1 5

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ACRTANACNG AYTGRYTAYTT NGT

23

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Thr Lys Tyr Gln Ser Val Tyr Val  
1 5

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GCDATNACRC AYTCTCYTT YTC

23

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Gly Phe Thr Trp Pro Gly Thr Phe  
1 5